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DEC 20 2002

TECH CENTER 1600/2900

## Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/717,789A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics  
Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ Misaligned Amino  
Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length  
Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0  
"bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences  
(OLD RULES)  
Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences  
(NEW RULES)  
Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☐ Use of n's or Xaa's  
(NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 ☐ Invalid <213>  
Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>  
Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0  
"bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

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1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/717,789A

DATE: 12/13/2002

TIME: 14:50:18

Input Set : A:\W160289.txt

Output Set: N:\CRF4\12132002\I717789A.raw

4 <110> APPLICANT: Chiorini, John  
 5 Kotin, Robert M.  
 6 Safer, Brian  
 8 <120> TITLE OF INVENTION: AAV5 VECTOR AND USES THEREOF  
 11 <130> FILE REFERENCE: 14014.0323U3  
 13 <140> CURRENT APPLICATION NUMBER: 09/717,789A  
 14 <141> CURRENT FILING DATE: 2000-11-21  
 17 <150> PRIOR APPLICATION NUMBER: PCT/US99/11958  
 18 <151> PRIOR FILING DATE: 1999-05-28  
 20 <150> PRIOR APPLICATION NUMBER: 60/087,029  
 21 <151> PRIOR FILING DATE: 1998-05-28  
 23 <160> NUMBER OF SEQ ID NOS: 24  
 25 <170> SOFTWARE: FastSEQ for Windows Version 3.0

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## ERRORED SEQUENCES

1069 <210> SEQ ID NO: 24  
 1070 <211> LENGTH: 735  
 1071 <212> TYPE: PRT  
 1072 <213> ORGANISM: Artificial Sequence  
 1074 <220> FEATURE:  
 1075 <223> OTHER INFORMATION: Description of Artificial Sequence:/Note =  
 1076 synthetic construct  
 1078 <400> SEQUENCE: 24  
 1079 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu  
 1080 1 5 10 15  
 1081 Ser Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro  
 E--> 1082 20 20 25 25 30 30  
 1083 Pro Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu  
 E--> 1084 35 40 45  
 1085 Pro Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu  
 E--> 1086 50 55 60  
 1087 Pro Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr  
 E--> 1088 65 70 75 80  
 1089 Asp Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His  
 E--> 1090 85 90 95  
 1091 Ala Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly  
 E--> 1092 100 105 110  
 1093 Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu  
 E--> 1094 115 120 125  
 1095 Pro Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys  
 E--> 1096 130 135 140

Does Not Comply  
Corrected Diskette Needed

pp 1-3

misaligned  
amino acid  
numbers  
(see item 3  
on Error  
Summary Sheet,

## RAW SEQUENCE LISTING

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TIME: 14:50:18

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```

1097 Arg Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr
E--> 1098 145 150 155 160
1099 Gly Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
E--> 1100 165 170 175
1101 Thr Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro
E--> 1102 180 185 190
1103 Pro Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser
E--> 1104 195 200 205
1105 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
E--> 1106 210 215 220
1107 Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val
E--> 1108 225 230 235 240
1109 Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
E--> 1110 245 250 255
1111 Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His
E--> 1112 260 265 270
1113 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
E--> 1114 275 280 285
1115 His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
E--> 1116 290 295 300
1117 Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
E--> 1118 305 310 315 320
1119 Val Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
E--> 1120 325 330 335
1121 Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro
E--> 1122 340 345 350
1123 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
E--> 1124 355 360 365
1125 Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
E--> 1126 370 375 380
1127 Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
E--> 1128 385 390 395 400
1129 Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
E--> 1130 405 410 415
1131 Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
E--> 1132 420 425 430
1133 Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
E--> 1134 435 440 445
1135 Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser
E--> 1136 450 455 460
1137 Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro
E--> 1138 465 470 475 480
1139 Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn
E--> 1140 485 490 495
1141 Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
E--> 1142 500 505 510
1143 Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
E--> 1144 515 520 525
1145 Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys

```

*same error*

*move this down to next line - Per 1.822 of sequence rules*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/717,789A

DATE: 12/13/2002

TIME: 14:50:18

Input Set : A:\W160289.txt

Output Set: N:\CRF4\12132002\I717789A.raw

```

E--> 1146      530      535      540
      1147 Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
E--> 1148 545      550      555      560
      1149 Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
E--> 1150      565      570      575
      1151 Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
E--> 1152      580      585      590
      1153 Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
E--> 1154      595      600      605
      1155 Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
E--> 1156      610      615      620
      1157 Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
E--> 1158 625      630      635      640
      1159 His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
E--> 1160      645      650      655
      1161 Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
E--> 1162      660      665      670
      1163 Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
E--> 1164      675      680      685
      1165 Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
E--> 1166      690      695      700
      1167 Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
E--> 1168 705      710      715      720
      1169 Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
E--> 1170      725      730      735

```

*same  
error*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/717,789A

DATE: 12/13/2002

TIME: 14:50:19

Input Set : A:\W160289.txt

Output Set: N:\CRF4\12132002\I717789A.raw

L:970 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1082 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:24  
M:332 Repeated in SeqNo=24